Control Of Gene Expression Section 11 1 Review Answers

Covers the progress in understanding the mechanisms for genomic control of gene expression. This book includes information on aspergillus genomes. It discusses sex and its role in virulence of human fungal pathogens. It also covers the genomic analysis of neurospora.
This is one of the first books that focuses on emerging concepts about the role of the structure of chromatin, the organization of the genome, and the structure of the interphase nucleus in the control of gene expression in eukaryotes. The first section analyses the relationship between the dynamic chromatin structure at the nucleosome level and gene expression. Section two looks into higher order chromatin structure in relation to transcription. In section three the molecular basis ofepigenetic phenomena, like X-chromosome inactivation is discussed, starting from our understanding of chromatin structure. Together, these topics form the molecular basis for our understanding of cell differentiation, knowledge that is essential for the design of transgenic animals and plants and for gene therapy in humans. The book is of direct interest to students that are new in the field and to investigators in the area of biomolecular sciences, like developmental biology, biochemistry, cell biology, microbiology and genetics. Also, those working in applied fields of research, i.e biotechnology and biomedicine, will strongly benefit from this book. It will help them to understand fundamental problems in transgenics and gene therapy. Importantly, a variety of human disorders may turn out to be caused by genetic or somatic errors related to this level of gene control.
Maximizing Gene Expression focuses on prokaryotic and eukaryotic gene expression. The book first discusses E. coli promoters. Topics include structure analysis, steps in transcription initiation, structure-function correlation, and regulation of transcription initiation. The text also highlights yeast promoters, including elements that select initiation sites, transcription regulation, regulatory proteins, and upstream promoter elements. The text also describes protein coding genes of higher eukaryotes; instability of messenger RNA in bacteria; and replication control of the ColE1-type plasmids. The text then describes translation initiation, including the translation of prokaryotes and eukaryotes. The book puts emphasis on the selective degradation of abnormal proteins in bacteria. Topics include proteins rapidly hydrolyzed in E. coli; intracellular aggregates of abnormal polypeptides; energy requirement and pathway for proteins; proteolytic enzymes in E. coli; and regulation of ion expression. The text also highlights the detection of proteins produced by recombinant DNA techniques and mechanism and practice. The book is a good source of information for readers wanting to study gene expression.
The text is appropriate for graduate student s reference and provides the essential groundwork for an advanced understanding of the various mechanisms that may result in altered activity of a specific cell protein in relation to gene expression. This book mainly focusing on two aspect, gene regulation and cell signaling regulation process. Part I focuses on approaches for studying control of mRNA expression and determining target genes for a given transcription copy and the methods for determining how proteins can regulate each other by mediating synthesis, degradation, protein-protein interactions, and posttranslational modification etc. Part II explores the different types of cell signaling process, signaling molecules and their mechanism.
The focus of this dissertation is the discovery of novel mechanisms and pathways of gene regulation by the aryl hydrocarbon receptor (AHR), primarily regarding the role of this protein in modulating cell cycle progression. The AHR is a member of the PAS (Per-Arnt-Sim) superfamily of receptors, which mediate responses to environmental stresses such as hypoxia and circadian rhythm, and control basic physiologic processes like vascular development,

learning, and neurogenesis. The AHR protein was discovered by virtue of its high affinity interaction with the persistent environmental contaminant 2,3,7,8-tetrachlorodibenzo- p-dioxin (TCDD), and is now known as the primary mediator of the toxic effects of this and hundreds of other HAH and PAH ligands. The mechanisms by which the AHR acts to mediate toxicity of these compounds include the activity of the AHR as a potent transcriptional activator. The ligand-bound AHR, with its dimerization-binding partner ARNT, upregulates the expression of a battery of genes that function in the metabolism of PAH and HAH compounds. However, the diversity of toxic responses mediated by compounds such as TCDD are not adequately explained by the expression of this battery of genes. One of the primary roles of the AHR, both from a physiological and toxicological standpoint, is the control of cell cycle progression. The AHR may affect cell proliferation, differentiation, or apoptosis depending on the cell type examined, and the mechanisms of these effects remain unclear. Literally hundreds of genes have been implicated as being regulated either directly or indirectly by the AHR, and many of these genes are related to aspects of cell cycle control. The goal of this dissertation is to explore mechanisms by which the AHR modulates the cell cycle through the investigation of novel gene targets of the receptor. Chapter 2 summarizes the current body of knowledge regarding the AHR, its ligands, and perturbations of the cell cycle. Chapter 3 investigates a mechanism whereby the AHR is able to repress the expression of specific cell cycle-regulated genes through its interaction with the retinoblastoma protein, a tumor suppressor and major component of the G1/S checkpoint control mechanism. Chapter 4 explores an interaction between the AHR and E2F proteins, also major regulatory components of S-phase progression and DNA replication, and the constitutive activity of the AHR in maintaining basal expression levels of a large number of E2F-regulated genes. Finally, Chapter 5 outlines the identification of novel promoter targets of the AHR using chromatin immunoprecipitation and promoter tiling arrays. The results presented throughout this work show the diversity of AHR functions related both to toxicological endpoints and normal cell physiology, and illustrate the ability of this important transcription factor to regulate the expression of a large number of genes by a variety of distinctive mechanisms.

The last ten years have witnessed a remarkable increase in our awareness of the importance of events subsequent to transcriptional initiation in terms of the regulation and control of gene expression. In particular, the development of recombinant DNA techniques that began in the 1970s provided powerful new tools with which to study the molecular basis of control and regulation at all levels. The resulting investigations revealed a diversity of post-transcriptional mechanisms in both prokaryotes and eukaryotes. Scientists working on translation, mRNA stability, transcriptional (anti)termination or other aspects of gene expression will often have met at specialist meetings for their own research area. However, only rarely do workers in different areas of post-transcriptional control/ regulation have the opportunity to meet under one roof. We therefore thought it was time to bring together leading representatives of most of the relevant areas in a small workshop intended to encourage interaction across the usual borders of research, both in terms of the processes studied, and with respect to the evolutionary division prokaryotes/eukaryotes. Given the breadth of topics covered and the restrictions in size imposed by the NATO workshop format, it was an extraordinarily difficult task to choose the participants. However, we regarded this first attempt as an experiment on a small scale, intended to explore the possibilities of a meeting of this kind. Judging by the response of the participants during and after the workshop, the effort had been worthwhile. The motivation for us to produce a treatise on regulation was mainly our convic tion that it would be fun, and at the same time productive, to approach the subject in a way that differs from that of other treatises. We had ourselves written reviews for various volumes over the years, most of them bringing together all possible facts relevant to a particular operon, virus, or biosynthetic system. And we were not convinced of the value of such reviews for anyone but

the expert in the field reviewed. We thought it might be more interesting and more instructive-for both author and reader-to avoid reviewing topics that anyone scientist might work on, but instead to review the various parts of what many different scientists work on. Cutting across the traditional boundaries that have separated the subjects in past volumes on regulation is not an easy thing to do-not because it is difficult to think of what interesting topics should replace the old ones, but because it is difficult to find authors who possess sufficient breadth of knowledge and who are willing to write about areas outside those pursued in their own laboratories. For example, no one scientist works on suppression per se. He may study the structure of suppressor tRNAs in Escherichia coli, he may study phenotypic suppression of various characters in drosophila, he may study polarity in gene expression, and so on.

Written in an informal and accessible style, Chromatin and Gene Regulation enables the reader to understand the science of this rapidly moving field. Chromatin is a fundamental component in the network of controls that regulates gene expression. Many human diseases have been linked to disruption of these control processes by genetic or environmental factors, and unravelling the mechanisms by which they operate is one of the most exciting and rapidly developing areas of modern biology. Chromatin is central both to the rapid changes in gene transcription by which cells respond to changes in their environment and also to the maintenance of gene expression patterns from one cell generation to the next. This book will be an invaluable guide to undergraduate and postgraduate students in the biological sciences and all those with an interest in the medical implications of aberrant gene expression.

RNA binding proteins are an exciting area of research in gene regulation. A multitude of RNA-protein interactions are used to regulate gene expression including pre-mRNA splicing, polyadenylation, editing, transport, cytoplasmic targeting, translation and mRNA turnover. In addition to these post-transcriptional processes, RNA-protein interactions play a key role in transcription as illustrated by the life cycle of retroviruses. Unlike DNA, the structure of RNA is highly variable and conformationally flexible, thus creating a number of unique binding sites and the potential for complex regulation by RNA binding proteins. Although there is a wide range of topics included in this volume, general themes have been repeated, highlighting the overall integrative nature of RNA binding proteins. The chapters have been separated into three different sections: Translational Control; mRNA Metabolism; and Hormonal and Homeostatic Regulation. The chapters of this volume were written with the seasoned investigator and student in mind. Summaries of key concepts are reviewed within each chapter as well as guiding questions that can be used to stimulate class discussions. The Editors of this volume hope that this compendium educates, enthralls, and stimulates the readers to look to the future possibilities in this rapidly evolving field.

Molecular Mechanisms in the Control of Gene Expression documents the proceedings of the ICN-UCLA conference on Molecular Mechanisms in the Control of Gene Expression, organized through the Molecular Biology Institute of UCLA, held in Keystone, Colorado, 21-26 March 1976. The conference focused

on three topics: the action of repressors on specific nucleotide sequences in DNA; how DNA and histones are intertwined in eucaryotic chromosomes; and in the development of new techniques that appear to lift genes from complex genomes. The volume contains 65 chapters organized into nine parts. The papers in Part I examine the organization of prokaryotic and eukaryotic chromosomes. Part II presents studies on the interaction of RNA a polymerase and regulatory molecules with defined DNA sites. Parts III and IV focus on RNA polymerases of eukaryotes and the regulation of transcription in eukaryotic systems, respectively. Part V contains papers dealing with nucleic acid sequences, transcription, and processing. Part VI covers cellular aspects in the study of gene expression. Part VII takes up cloning while Part VIII is devoted to genetic analysis through restriction mapping and molecular cloning. Finally, Part IX summarizes the recent progress reported at the conference and also indicates some of the limitations that can be placed upon interpretation of data.

The new edition of Gene Control has been updated to include significant advances in the roles of the epigenome and regulatory RNAs in gene regulation. The chapter structure remains the same: the first part consists of pairs of chapters that explain the mechanisms involved and how they regulate gene expression, and the second part deals with specific biological processes (including diseases) and how they are controlled by genes. Coverage of methodology has been strengthened by the inclusion more explanation and diagrams.The significant revision and updating will allow Gene Control to continue to be of value to students, scientists and clinicians interested in the topic of gene control.

The eukaryotic gene expression pathway involves a number of interlinked steps, with messenger RNA (mRNA) being the key intermediate. The precursor mRNA is transcribed from DNA, processed by removal of introns and addition of the cap structure and the poly(A) tail. The mature mRNA is then exported to the cytoplasm where it is translated into protein and finally degraded. In this process, mRNA is associated with RNA-binding proteins forming ribonucleoprotein complexes, whose protein content evolves throughout the lifetime of the mRNA. While the complexity of eukaryotic gene expression allows the production of proteins to be controlled at many levels, it also makes the process vulnerable to errors. Although eukaryotic cells have evolved elaborate mRNA quality control mechanisms that ensure the fidelity of gene expression, some defects are not detected, thus affecting mRNA metabolism. This condition plays a fundamental role in the pathogenesis of several disease processes, such as neurodegeneration and oncogenesis. Besides, exciting recent data have shown that cellular RNAs can be modified post-transcriptionally via dynamic and reversible chemical modifications, the so-called epitranscriptome. These modifications can alter mRNA structure, being able to modulate different steps of the mRNA metabolism that can be associated with various human diseases, such as systemic lupus erythematosus and cancer. This book provides a

collection of novel studies and hypotheses aimed to define the pathophysiological consequences of altered mRNA metabolism events in human cells, and is written for a wide spectrum of readers in the field of gene expression regulation. The last chapter highlights how the discovery of disease-causing defects (or modifications) in mRNA can provide a variety of therapeutic targets that can be used for the development of new RNA-based therapeutics. Hopefully, it may also contribute to inspire the drug-developing scientific community.

Abstract: NF-kB was discovered over 20 years ago, and while the knowledge of this transcription factor has been considerably expanded, it is still not completely understood how a single signaling pathway regulates such a diverse array of events in cells. One of the ways in which this transcription factor may target a variety of genes under different conditions is through post-translational modifications that regulate how the complex binds to gene promoters, as well as how it binds to other co-factors. This thesis is designed to investigate how these modifications, specifically phosphorylation, regulate gene expression and control NF-kB mediated events. Chapter one is a general introduction to NF-kB, and also discusses some of the known NF-kB target genes as well as diseases that are known to occur at least in part due to deregulated NF-kB activity. Chapter two investigates the effect of phosphorylation on the stability of IkBb, an inhibitor of NF-kB. We show that this regulation is important for maintenance of normal cell growth in mouse embryo fibroblasts. Chapters three and four focus on a different aspect of phosphorylation. In contrast to how protein phosphorylation controls stability, these chapters are designed specifically to determine how this modification affects target gene transcription. The goal of this part of the thesis is to further elucidate whether specific phosphorylation at particular resides can differentially affect sub-sets of endogenous genes. Finally, chapter five discusses the attempts to determine the role of NF-kB post-translation modification in other cell types, as well as discuss the importance of increasing our current knowledge as to how this complicated transcription factor signals. Insight into how NF-kB differentially regulates subsets of genes may allow for development of specific therapeutic targets. Currently, drugs that inhibit NF-kB on a broad level are in use, however these types of treatments may have undesirable side effects due to non-specific inhibition of other beneficial pathways in the cell. The ability to develop more specific inhibitors that affect only a small number of genes important in a particular disease will allow for more efficient therapies.

This book presents some of the most recent, novel and fascinating examples of transcriptional and posttranscriptional control of gene expression in plants and, where appropriate, provides comparison to notable examples of animal gene regulation.

Levels of gene control -- Structure of chromatin -- Role of chromatin structure in gene control -- The process of transcription -- Transcription factors and transcriptional control -- Post-transcriptional processes -- Post-transcriptional regulation -- Gene control and cellular signaling pathways -- Gene control in

embryonic development -- Control of cell-type-specific gene expression -- Gene regulation and cancer -- Gene regulation and human disease -- Conclusions and future prospects.

Non-coding RNAs potentially play an active role in modulating gene transcription and epigenetic states. Several genes in differentiated cells may be under some form of RNA-based transcriptional and epigenetic regulatory control. This form of regulation may be controlled by selective pressures and influence the adaptability of the cell. The concept that RNA can control epigenetic states impacts our understanding of the basic fabric of the cell and may have therapeutic potential. Many studies have been carried out on the modulation of gene transcription by non-coding RNAs. This book, written by a group of distinguished scientists, represents an important overview and summary of the field to date. The 13 chapters are organized into three sections: a) Non-coding RNAs: Form, Function and Diversity; b) Non-coding RNAs: Gene Regulation and Epigenetics; and c) Non-coding RNAs: Disease and Therapeutics. This up-to-date volume is an essential book for those working in the area and represents a major information resource on current research in the fast-moving fields of epigenetics, the regulation of gene expression, and RNA research.

A much-needed guide through the overwhelming amount of literature in the field. Comprehensive and detailed, this book combines background information with the most recentinsights. It introduces current concepts, emphasizing the transcriptional control of genetic information. Moreover, it links data on the structure of regulatory proteins with basic cellular processes. Both advanced students and experts will find answers to such intriguing questions as: - How are programs of specific gene repertoires activated and controlled? - Which genes drive and control morphogenesis? - Which genes govern tissue-specific tasks? - How do hormones control gene expression in coordinating the activities of different tissues? An abundant number of clearly presented glossary terms facilitates understanding of the biological background. Speacial feature: over 2200 (!) literature references.

The OHOLO Conferences have been convened annually from the Spring of 1956; the wide areas they have covered, from different and overlapping disciplines, can be seen from the following list: 1956 Bacterial Genetics (not published) 1957 Tissue Cultures in Virological Research (not published) 1958 Inborn and Acquired Resistance to Infection in Animals (not published) 1959 Experimental Approach to Mental Diseases (not published) 1960 Cryptobiotic Stages in Biological Systems* 1961 Virus-Cell Relationships** 1962 Biological Synthesis and Function of Nucleic Acids** 1963 Cellular Control Mechanism of Macromolecular Synthesis** 1964 Molecular Aspects of Immunology** 1965 Cell Surfaces** 1966 Chemistry and Biology of Psychotropic Agents (not published) 1967 Structure and Mode of Action of Enzymes** 1968 Growth and Differentiation of Cells In Vitro** 1969 Behaviour of Animal Cells in Culture** 1970 Microbial Toxins** 1971 Interaction of Chemical Agents with Cholinergic

Mechanisms** 1972 Immunity in Viral and Rickettsial Diseases*** The participants who attend these Conferences are drawn from dif ferent scientific institutions in Israel and from many foreign countries; they are engaged in fields of study which represent widely divergent approaches to biology. Thus a distinguishing feature of the OHOLO meetings has been their multi-disciplinary nature. Published by Elsevier Publishing Co. , Amsterdam (1960). * ** Published by the Israel Institute for Biological Research, Ness Ziona. *** Published by Plenum Press, New York (1972). ix PREFACE x These small international conferences are also characterized by their relaxed atmosphere, with ample time for informal as well as formal discussions.

The use of molecular biology and biochemistry to study the regulation of gene expression has become a major feature of research in the biological sciences. Many excellent books and reviews exist that examine the experimental methodology employed in specific areas of molecular biology and regulation of gene expression. However, we have noticed a lack of books, especially textbooks, that provide an overview of the rationale and general experimental approaches used to examine chemically or disease-mediated alterations in gene expression in mammalian systems. For example, it has been difficult to find appropriate texts that examine specific experimental goals, such as proving that an increased level of mRNA for a given gene is attributable to an increase in transcription rates. Regulation of Gene Expression: Molecular Mechanisms is intended to serve as either a textbook for graduate students or as a basic reference for laboratory personnel. Indeed, we are using this book to teach a graduate-level class at The Pennsylvania State University. For more details about this class, please visit http://moltox. cas. psu. edu and select “Courses. ” The goal for our work is to provide an overview of the various methods and approaches to characterize possible mechanisms of gene regulation. Further, we have attempted to provide a framework for students to develop an understanding of how to determine the various mechanisms that lead to altered activity of a specific protein within a cell.

Plant Genes, Genomes and Genetics provides a comprehensive treatment of all aspects of plant gene expression. Unique in explaining the subject from a plant perspective, it highlights the importance of key processes, many first discovered in plants, that impact how plants develop and interact with the environment. This text covers topics ranging from plant genome structure and the key control points in how genes are expressed, to the mechanisms by which proteins are generated and how their activities are controlled and altered by posttranslational modifications. Written by a highly respected team of specialists in plant biology with extensive experience in teaching at undergraduate and graduate level, this textbook will be invaluable for students and instructors alike. Plant Genes, Genomes and Genetics also includes: specific examples that highlight when and how plants operate differently from other organisms special sections that provide in-depth discussions of particular issues end-of-chapter problems to help

students recapitulate the main concepts rich, full-colour illustrations and diagrams clearly showing important processes in plant gene expression a companion website with PowerPoint slides, downloadable figures, and answers to the questions posed in the book Aimed at upper level undergraduates and graduate students in plant biology, this text is equally suited for advanced agronomy and crop science students inclined to understand molecular aspects of organismal phenomena. It is also an invaluable starting point for professionals entering the field of plant biology.

Bacteria in various habitats are subject to continuously changing environmental conditions, such as nutrient deprivation, heat and cold stress, UV radiation, oxidative stress, dessication, acid stress, nitrosative stress, cell envelope stress, heavy metal exposure, osmotic stress, and others. In order to survive, they have to respond to these conditions by adapting their physiology through sometimes drastic changes in gene expression. In addition they may adapt by changing their morphology, forming biofilms, fruiting bodies or spores, filaments, Viable But Not Culturable (VBNC) cells or moving away from stress compounds via chemotaxis. Changes in gene expression constitute the main component of the bacterial response to stress and environmental changes, and involve a myriad of different mechanisms, including (alternative) sigma factors, bi- or tri-component regulatory systems, small non-coding RNA’s, chaperones, CHRIS-Cas systems, DNA repair, toxin-antitoxin systems, the stringent response, efflux pumps, alarmones, and modulation of the cell envelope or membranes, to name a few. Many regulatory elements are conserved in different bacteria; however there are endless variations on the theme and novel elements of gene regulation in bacteria inhabiting particular environments are constantly being discovered. Especially in (pathogenic) bacteria colonizing the human body a plethora of bacterial responses to innate stresses such as pH, reactive nitrogen and oxygen species and antibiotic stress are being described. An attempt is made to not only cover model systems but give a broad overview of the stress-responsive regulatory systems in a variety of bacteria, including medically important bacteria, where elucidation of certain aspects of these systems could lead to treatment strategies of the pathogens. Many of the regulatory systems being uncovered are specific, but there is also considerable “cross-talk” between different circuits. Stress and Environmental Regulation of Gene Expression and Adaptation in Bacteria is a comprehensive two-volume work bringing together both review and original research articles on key topics in stress and environmental control of gene expression in bacteria. Volume One contains key overview chapters, as well as content on one/two/three component regulatory systems and stress responses, sigma factors and stress responses, small non-coding RNAs and stress responses, toxin-antitoxin systems and stress responses, stringent response to stress, responses to UV irradiation, SOS and double stranded systems repair systems and stress, adaptation to both oxidative and osmotic stress, and desiccation tolerance and drought stress. Volume Two covers heat

shock responses, chaperonins and stress, cold shock responses, adaptation to acid stress, nitrosative stress, and envelope stress, as well as iron homeostasis, metal resistance, quorum sensing, chemotaxis and biofilm formation, and viable but not culturable (VBNC) cells. Covering the full breadth of current stress and environmental control of gene expression studies and expanding it towards future advances in the field, these two volumes are a one-stop reference for (non) medical molecular geneticists interested in gene regulation under stress.

The expression of a gene begins by transcribing a target region on the DNA to form a molecule of messenger RNA. As transcription is the first step of gene expression, it is there- fore highly regulated. The regulation of transcription is essential in fundamental biological processes, such as cell growth, development and differentiation. The process is carried out by an enzyme, RNA polymerase, which catalyzes the addition of a nucleotide complementary to the template and moves along the DNA one base pair at a time. To complete its tasks, the enzyme functions as a complex molecular machine, possessing various evolutionarily designed parts. In eukaryotes, RNA polymerase has to transcribe through DNA wrapped around histone proteins forming nucleosomes. These structures represent physical barriers to the transcribing enzyme. In chapter 2, we investigated how each nucleosomal component--the histone tails, the specific histone-DNA contacts, and the DNA sequence--contributes to the strength of the barrier. Removal of the tails favors progression of RNA polymerase II into the entry region of the nucleosome by locally increasing the wrapping-unwrapping rates of the DNA around histones. In contrast, point mutations that affect histone-DNA contacts at the dyad abolish the barrier to transcription in the central region by decreasing the local wrapping rate. Moreover, we showed that the nucleosome amplifies sequence-dependent transcriptional pausing, an effect mediated through the structure of the nascent RNA. Each of these nucleosomal elements controls transcription elongation by distinctly affecting the density and duration of polymerase pauses, thus providing multiple and alternative mechanisms for control of gene expression by additional factors. During transcription elongation, RNA polymerase has been assumed to attain equilibrium between pre- and post-translocated states rapidly relative to the subsequent catalysis. Under this assumption, a branched Brownian ratchet mechanism that necessitates a putative secondary nucleotide binding site on the enzyme was proposed. In chapter 3, we challenged individual yeast RNA polymerase II (Pol II) with a nucleosome as a "road block", and separately measured the forward and reverse translocation rates with our single-molecule transcription elongation assay. Surprisingly, we found that the forward translocation rate is comparable to the catalysis rate. This finding reveals a linear, non-branched ratchet mech-anism for the nucleotide addition cycle in which translocation is one of the rate-limiting steps. We further determined all the major on- and off-pathway kinetic parameters in the elongation cycle. This kinetic model provides a framework to study the influence of various factors on

transcription dynamics. To further dissect the operation of Pol II, we focused on the trigger loop, a mobile element near the active site of the enzyme. Biochemical and structural studies have demonstrated that the trigger loop makes direct contacts with substrates and promotes nucleotide incorporation. It is also an important regulatory element for transcription fidelity. In chapter 4, we characterized the dynamics of a trigger loop mutant RNA polymerase to elucidate the roles of this element in transcription regulation, and applied the above kinetic framework to quantify the effects of the mutation. In comparison to the wild-type enzyme, we found that the mutant is more sensitive to force, faster at substrate sequestration, and more efficient to return from a pause to active transcription. This work highlighted important roles of regulatory elements in controlling transcription dynamics and fidelity. Moreover, RNA polymerase interacts with various additional factors, which add layers of regulation on transcription. Transcription factors IIS (TFIIS) and IIF (TFIIF) are known to interact with elongating RNA polymerase directly and stimulate transcription. In chapter 5, we studied the effects of these factors on elongation dynamics using our single molecule assay. We found that both TFIIS and TFIIF enhance the overall transcription elongation by reducing the lifetime of transcriptional pauses and that TFIIF also decreases the probability of pause entry. Furthermore, we observed that both factors enhance the efficiency of nucleosomal transcription. Our findings helped elucidate the molecular mechanisms of gene expression modulation by transcription factors. In summary, we have dissected the mechanisms by which the nucleosomal elements regulate transcription, and derived a quantitative kinetic model of transcription elongation in a linear Brownian ratchet scheme with the slow translocation of the enzyme. The corresponding translocation energy landscape shows that the off-pathway states are favored thermodynamically but not kinetically over the on-pathway states. This observation confers the enzyme its high propensity to pause, thus allowing additional regulatory mechanisms during pausing. TFIIS and TFIIF, for example, regulate transcription dynamics by shortening the lifetime of Pol II pauses. On the other hand, the trigger loop of Pol II regulates both the active elongation and pausing. These examples illustrate molecular mechanisms of cis- and trans-acting factors regulate the dynamics of transcription elongation.

This is the first comprehensive review of mRNA stability and its implications for regulation of gene expression. Written by experts in the field, Control of Messenger RNA Stability serves both as a reference for specialists in regulation of mRNA stability and as a general introduction for a broader community of scientists. Provides perspectives from both prokaryotic and eukaryotic systems Offers a timely, comprehensive review of mRNA degradation, its regulation, and its significance in the control of gene expression Discusses the mechanisms, RNA structural determinants, and cellular factors that control mRNA degradation Evaluates experimental procedures for studying mRNA degradation

Sixty years after the "central dogma," great achievements have been developed

in molecular biology. We have also learned the important functions of noncoding RNAs and epigenetic regulations. More importantly, whole genome sequencing and transcriptome analyses enabled us to diagnose specific diseases. This book is not only intended for students and researchers working in laboratory but also physicians and pharmacists. This volume consists of 14 chapters, divided into 4 parts. Each chapter is written by experts investigating biological stresses, epigenetic regulation, and functions of transcription factors in human diseases. All articles presented in this volume by excellent investigators provide new insights into the studies in transcriptional control in mammalian cells and will inspire us to develop or establish novel therapeutics against human diseases.
This book is the first volume in a new series Progress in Gene Expres sion. The control of gene expression is a central-most topic in molecular biology as it deals with the utilization and regulation of gene informa tion. As we see huge efforts mounting all over the developed world to understand the structure and organization of several complex eukaryotic genomes in the form of Gene Projects and Genome Centers, we have to remember that without understanding the basic mechanisms that gov ern the use of genetic information, much of this effort will not be very productive. Fortunately, however, research during the past seven years on the mechanisms that control gene expression in eukaryotes has been extremely successful in generating a wealth of information on the basic strategies of transcriptional control. (Although regulation of gene ex pression is exerted at many different levels, much of the emphasis in this series will be on transcriptional control. A future volume, however, will deal with other levels of regulation). The progress in understanding the control of eukaryotic transcription can only be appreciated by realizing that seven years ago we did not know the primary structure of a single sequence specific transcriptional activator, and those whose primary structures were available (e. g. , homeo domain proteins) were not yet recognized to function in this capacity.
"Genetics: From Genes to Genomes" is a cutting-edge, introductory genetics text authored by an unparalleled author team, including Nobel Prize winner, Leland Hartwell. The Third Edition continues to build upon the integration of Mendelian and molecular principles, providing students with the links between early genetics understanding and the new molecular discoveries that have changed the way the field of genetics is viewed.
'I therefore regard this book as a standard, extremely suitable not only for teaching to 3rd or 4th year undergraduate students with interest in cellular biology and molecular microbiology, but also for senior scientists who have research interests in prokaryotic transcription regulation2 Cell Biology International'a superb, compact yet comprehensive, treatise on the regulation of gene expression, principally but not exclusively, in E.Coli and its phage... A must for all students at undergraduate or postgraduate level and also for reseachers of eukaryotic transcription who need reminding of a few paradigms' AslibThis text is written for advanced students with a basic background in molecular biology and

provides a clear and concise summary of the flow of information from genes to proteins in simple prokaryotic cells. Transcription regulation is of central importance to molecular biology, and in bacterial cells the major regulatory stage is transcription. While most textbooks cover transcription in a single chapter with a strong emphasis on eukaryotic transcription, this new text is devoted to prokaryotic transcription and is perfect for use on molecular biology, microbiology and technology courses.

Transcription factors are the molecules that the cell uses to interpret the genome: they possess sequence-specific DNA-binding activity, and either directly or indirectly influence the transcription of genes. In aggregate, transcription factors control gene expression and genome organization, and play a pivotal role in many aspects of physiology and evolution. This book provides a reference for major aspects of transcription factor function, encompassing a general catalogue of known transcription factor classes, origins and evolution of specific transcription factor types, methods for studying transcription factor binding sites in vitro, in vivo, and in silico, and mechanisms of interaction with chromatin and RNA polymerase.

Regulation of Gene ExpressionSpringer Science & Business Media

A recent volume of this series (Signals and Signal Transduction Pathways in Plants (K. Palme, ed.) Plant Molecular Biology 26, 1237-1679) described the relay races by which signals are transported in plants from the sites of stimuli to the gene expression machinery of the cell. Part of this machinery, the transcription apparatus, has been well studied in the last two decades, and many important mechanisms controlling gene expression at the transcriptional level have been elucidated. However, control of gene expression is by no means complete once the RNA has been produced. Important regulatory devices determine the maturation and usage of mRNA and the fate of its translation product. Post-transcriptional regulation is especially important for generating a fast response to environmental and intracellular signals. This book summarizes recent progress in the area of post-transcriptional regulation of gene expression in plants. 18 chapters of the book address problems of RNA processing and stability, regulation of translation, protein folding and degradation, as well as intracellular and cell-to-cell transport of proteins and nucleic acids. Several chapters are devoted to the processes taking place in plant organelles.

Microbial cells can be manipulated to produce valuable chemicals and products. Cyanobacteria are an attractive candidate for conversion of CO2 into useful products because of their fast generation time and ability to be cultivated on non-arable land. In other organisms as well as in cyanobacteria, metabolic engineering efforts and strategies are heavily reliant on the underlying genetic tools that facilitate changes in gene expression of both native and exogenous biochemical pathways. One relatively unexplored area in terms of manipulating gene expression is transcript stability. This thesis expands the toolset for manipulating gene expression in cyanobacteria and probes the relatively unexplored area of RNA stability. The ribonucleases that mediate RNA turnover in cyanobacteria are analyzed, and the functions of three RNase III enzymes are described. A global RNA turnover study using RNA-sequencing showed that RNA turnover was very rapid and identified preliminary links between transcript

stability and sequence elements that may confer stability. Finally, genetic tools were built to control gene expression in cyanobacteria and applied to increase lactate production. These genetic tools and findings on RNA turnover in cyanobacteria provide significant advances towards reliable prediction and engineering of a synthetic transcript.

"Post-transcriptional control is a critical determinant of gene expression that acts at the level of the messenger RNA (mRNA), which includes processes such as translational control and RNA localization, and is the focus of this thesis. This regulation is in part dictated by the characteristics of the 5' and 3' untranslated regions (UTRs) of the mRNA and the cis-elements they harbour. Translational control can occur at the initiation step where the 5' cap structure of the mRNA is recognized by the eIF4E, whose activity can be modulated by the eIF4E-binding protein (4E-BP), a repressor of translation. The target of rapamycin (TOR) pathway integrates a plethora of signals and impinges on protein synthesis through its action on 4E-BPs and S6 kinases (S6Ks), two well-characterized targets. The TOR/4E-BP/eIF4E axis is known to regulate the translation of subsets of mRNAs with distinct features in their 5'UTRs. In light of recent work that demonstrated dysregulated translation of specific mRNAs in the brains of mice lacking 4E-BP2 and engendering autism spectrum disorder-like phenotypes, we endeavoured to similarly identify mRNAs regulated by d4E-BP in Drosophila. In Chapter 2, we performed ribosome profiling to identify specific mRNAs that are translationally regulated downstream of d4E-BP in the adult fly head, used as a proxy for the brain. Gene ontology (GO) analysis revealed that the corresponding genes of some of the upregulated mRNAs are involved in innate immunity. We determined that upregulated mRNAs possess 5'UTRs that are shorter but more complex. In our effort to validate one of the targets, dS6K, we detected elevated levels of p-RPS6, a readout of dS6K activity, in d4E-BPnull flies. We conclude there are subsets of differentially ribosome-associated mRNAs with distinct 5'UTR features in the d4E-BPnull fly head.Subcellular localization of mRNAs in the Drosophila embryo establishes a molecular asymmetry of maternally-inherited determinants that is essential for its development. Of the hundreds of transcripts that localize to the primordial germ cells at the posterior of the early embryo, only 55 RNAs accumulate around posterior nuclei prior to the development of those cells, termed RNA islands. Many of the genes that encode these mRNAs have established functions in embryonic patterning and germline development. Despite their common destination to RNA islands, a shared localization element has yet to be identified. In Chapter 3, we mapped the localization elements within the 3'UTRs of two transcripts that localize to RNA islands, polar granule component (pgc) and germ cell-less (gcl). Based on deletion mutation analysis, we report that gcl has redundant localization elements, while pgc possesses a localization element in the distal region. We show that the localization of polar granule proteins, Oskar, Tudor and Vasa, and 11 RNAs have conserved posterior localization in Drosophilids. Using recent findings of a sequence motif that contributes to RNA island localization, we found that this motif is enriched in the 3'UTRs of the majority of transcripts that localize in this way. Our data suggests that the RNA island type of posterior localization is an important process for directing the localization of transcripts with key roles in germline development, as highlighted by the many aspects of this process that is conserved"--

In Post-Transcriptional Gene Regulation, renowned authors present current technical approaches to most aspects of post-transcriptional control and provide a useful and versatile laboratory bench resource. With chapters split into sections covering bioinformatics, fundamental aspects of the study of RNA biology, and techniques for specific aspects of RNA biology, the expert authors have filled the book with invaluable tricks of the trade, perfected in their state-of-the-art laboratories. This new volume from the Methods in Molecular Biology series is convinently divided into three sections. The first section presents a series of bioinformatic approaches to address the use of RNA databases and algorithms to the study of post-transcriptional regulation involving untranslated regions of transcripts. In the second section, a series of methods applicable to fundamental issues in mRNA biology are presented. These include RNA structure/function, mRNP analysis and novel methods for mRNA labeling and isolation. The third section of this volume presents methodologies to study particular aspects of post-transcriptional control. This section includes methods for the study of alternative splicing and 3' end processing, mRNA localization, mRNA translation, mRNA stability and si/miRNA regulation. Collectively, Post-Transcriptional Gene Regulation provides the reader with a useful and versatile laboratory bench resource that will become an essential reference in the field.

There is fresh interest in protein synthesis and recognition of the key role of translational control mechanisms in regulating gene expression. This new monograph updates and expands the scope of the 1996 publication, Translational Control, but it also takes a fresh look at the field. In a new format, the first eight chapters provide broad overviews, while each of the additional twenty-eight has a focus on a research topic of more specific interest. The result is a thoroughly up-to-date account of initiation, elongation, and termination of translation, control mechanisms in development in response to extracellular stimuli, and the effects on the translational machinery of virus infection and disease. This book is essential reading for students entering the field and an invaluable resource for investigators of gene expression and its control.

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